

Exhibit II


Query: SEQ ID NO: 8

## BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search](#) [Strategies](#) [Formatting options](#) [Download](#)

### Nucleotide Sequence (19 letters)

Results for: lcl|9600 None(19bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|9600

Description

None

Molecule type

nucleic acid

Query Length

19

Database Name

nr

Description

All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)

### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Distance tree of results](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

### Database

Posted date	Dec 28, 2008 5:47 PM
Number of letters	252,991,180
Number of sequences	7,851,115
Entrez query	none

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

## Results Statistics

Length adjustment	17
Effective length of query	2
Effective length of database	25589522225
Effective search space	51179044450
Effective search space used	51179044450

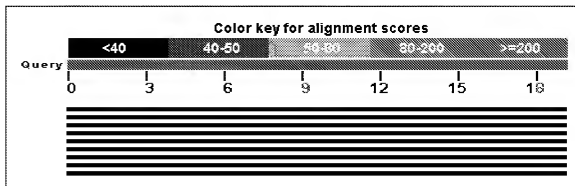
**New** Designing or Testing PCR Primers? Try your s

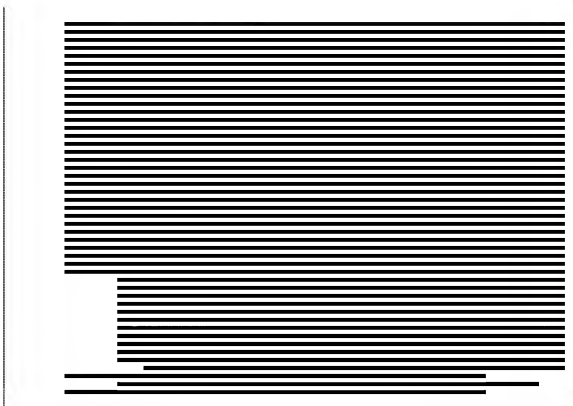
## Graphic Summary

### Distribution of 112 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





## Descriptions

Legend for links to other resources: [U](#) UniGene [G](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

XM_001916096.1	PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA	38.2	38.2	100%	0.17	100%	<a href="#">G</a>
NM_001115119.1	Canis lupus familiaris glutathione peroxidase 1 (GPX1), mRNA	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
XR_038530.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	38.2	38.2	100%	0.17	100%	<a href="#">G</a>
XR_038228.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	38.2	38.2	100%	0.17	100%	<a href="#">G</a>
NM_001077512.2	Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA	38.2	38.2	100%	0.17	100%	<a href="#">G</a>
AK239914.1	Sus scrofa mRNA, clone:UTR010010607, expressed in uterus	38.2	38.2	100%	0.17	100%	<a href="#">U</a>
AK231261.1	Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine	38.2	38.2	100%	0.17	100%	<a href="#">U</a>
AB121000.1	Callithrix jacchus gp1 mRNA for glutathione peroxidase 1, complete cds	38.2	38.2	100%	0.17	100%	
AB120996.1	Pan troglodytes gp1 mRNA for glutathione peroxidase 1, complete cds	38.2	38.2	100%	0.17	100%	<a href="#">G</a>
AK225835.1	Homo sapiens mRNA for Glutathione peroxidase 1 variant, clone: FCC127C01	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
XR_013650.1	PREDICTED: Macaca mulatta similar to Glutathione peroxidase 1 (GSHPx-1) (GPX-1) (Cellular glutathione peroxidase) (LOC706732), mRNA	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
AY966403.1	Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA, complete cds	38.2	38.2	100%	0.17	100%	
AY743601.1	Sus scrofa cytosolic glutathione peroxidase mRNA, partial cds	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
BC007865.2	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:14399 IMAGE:4301275), complete cds	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
BC000742.2	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:2335 IMAGE:3505654), complete cds	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
BC070258.1	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:88245 IMAGE:6452792), complete cds	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
AY572225.1	Canis familiaris glutathione peroxidase 1 mRNA, partial cds	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>
AC135371.2	Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence	38.2	38.2	100%	0.17	100%	
AY327818.1	Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cds	38.2	38.2	100%	0.17	100%	<a href="#">G</a>
NM_214201.1	Sus scrofa glutathione peroxidase 1	38.2	38.2	100%	0.17	100%	<a href="#">U</a> <a href="#">G</a>

**Now** Designing or Testing PCR Primers? Try your s

Alignments Select All Get selected sequences Distance tree of results

>ref|XM\_001916096.1| **G** PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA  
Length=606

GENE ID: 100053396 LOC100053396 | similar to glutathione peroxidase 1 [Equus caballus]

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 322    TGAAGTTGGGCTCGAACCC 304
```

>ref|NM\_001115119.1| **UEG** Canis lupus familiaris glutathione peroxidase 1 (GPX1)  
Length=838

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 343    TGAAGTTGGGCTCGAACCC 325
```

>ref|XR\_038530.1| **G** PREDICTED: Homo sapiens misc\_RNA (LOC441481), miscRNA  
Length=876

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 361    TGAAGTTGGGCTCGAACCC 343
```

>ref|XR\_038228.1| **G** PREDICTED: Homo sapiens misc\_RNA (LOC441481), miscRNA  
Length=878

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 38.2 bits (19), Expect = 0.17

Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 363 TGAAGTTGGGCTCGAACCC 345

>ref|NM\_001077512.2| **G** Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA  
Length=613

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]  
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 329 TGAAGTTGGGCTCGAACCC 311

>dbj|AK239914.1| **G** Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus  
Length=912

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 420 TGAAGTTGGGCTCGAACCC 402

>dbj|AK231261.1| **G** Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine  
Length=936

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 435 TGAAGTTGGGCTCGAACCC 417

>dbj|AB121000.1| Callithrix jacchus gpx1 mRNA for glutathione peroxidase 1, comp  
cds  
Length=606

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>dbj|AB120996.1| **G** Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, compl  
cds  
Length=606

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]  
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||

Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>dbj|AK225835.1| **UG** Homo sapiens mRNA for Glutathione peroxidase 1 variant, cloc  
FCC127C01  
Length=874

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 331 TGAAGTTGGGCTCGAACCC 313

>ref|XR\_013650.1| **UG** PREDICTED: Macaca mulatta similar to Glutathione peroxidase  
(GSHPx-1) (GPX-1) (Cellular glutathione peroxidase) (LOC706732),  
mRNA  
Length=811

GENE ID: 706732 LOC706732 | similar to Glutathione peroxidase 1 (GSHPx-1)  
(GPX-1) (Cellular glutathione peroxidase) [Macaca mulatta]

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 313 TGAAGTTGGGCTCGAACCC 295

>gb|AY966403.1| Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA  
complete cds  
Length=858

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 345 TGAAGTTGGGCTCGAACCC 327

>gb|AY743601.1| **UG** Sus scrofa cytosolic glutathione peroxidase mRNA, partial cd  
Length=256

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]  
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 95 TGAAGTTGGGCTCGAACCC 77

>gb|BC007865.2| **UG** Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:  
IMAGE:4301275), complete cds  
Length=851

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)

```

Strand=Plus/Minus

Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 338    TGAAGTTGGGCTCGAACCC 320

>gb|BC000742.2| UEG Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG
IMAGE:3505654), complete cds
Length=863

  GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
  (Over 100 PubMed links)

  Score = 38.2 bits (19), Expect = 0.17
  Identities = 19/19 (100%), Gaps = 0/19 (0%)
  Strand=Plus/Minus

Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 351    TGAAGTTGGGCTCGAACCC 333

>gb|BC070258.1| UEG Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG
IMAGE:6452792), complete cds
Length=866

  GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
  (Over 100 PubMed links)

  Score = 38.2 bits (19), Expect = 0.17
  Identities = 19/19 (100%), Gaps = 0/19 (0%)
  Strand=Plus/Minus

Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 344    TGAAGTTGGGCTCGAACCC 326

>gb|AY572225.1| UG Canis familiaris glutathione peroxidase 1 mRNA, partial cds
Length=434

  GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

  Score = 38.2 bits (19), Expect = 0.17
  Identities = 19/19 (100%), Gaps = 0/19 (0%)
  Strand=Plus/Minus

Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 283    TGAAGTTGGGCTCGAACCC 265

>gb|AC135371.2| B Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute
Human BAC Library) complete sequence
Length=25901

  Score = 38.2 bits (19), Expect = 0.17
  Identities = 19/19 (100%), Gaps = 0/19 (0%)
  Strand=Plus/Plus

Query 1      TGAAGTTGGGCTCGAACCC 19
            |||
Sbjct 8885   TGAAGTTGGGCTCGAACCC 8903

>gb|AY327818.1| G Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cd
Length=4877

  GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
  (Over 100 PubMed links)

```



Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 2772 TGAAGTTGGGCTCGAACCC 2754

>ref|NM\_214201.1| **UG** Sus scrofa glutathione peroxidase 1 (GPX1), mRNA  
 gb|AF532927.1| **UG** Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, com  
 cds  
 Length=803

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]  
 (10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 343 TGAAGTTGGGCTCGAACCC 325

>dbj|AB120999.1| Cebus apella gpx1 mRNA for glutathione peroxidase 1, complete  
 cds  
 Length=606

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>dbj|AB120998.1| Hylobates lar gpx1 mRNA for glutathione peroxidase 1, complete  
 cds  
 Length=606

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>dbj|AB120997.1| Pongo pygmaeus gpx1 mRNA for glutathione peroxidase 1, complete  
 cds  
 Length=606

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>gb|M83094.1|HUMGLPEX **EG** Homo sapiens cytosolic selenium-dependent glutathione  
 gene, complete cds, and rhoh12 gene, 3' end  
 Length=4407

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||  
 Sbjct 3157 TGAAGTTGGGCTCGAACCC 3139

>emb|Y00483.1|HSGSHPXG **EG** Human gene for glutathione peroxidase  
 Length=1733

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||  
 Sbjct 1073 TGAAGTTGGGCTCGAACCC 1055

>emb|Y00433.1|HSGSHPX **UEG** Human mRNA for glutathione peroxidase (EC 1.11.1.9.)  
 Length=1134

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||  
 Sbjct 640 TGAAGTTGGGCTCGAACCC 622

>emb|X13710.1|HSPEROXP **UEG** H.sapiens unspliced mRNA for glutathione peroxidase  
 Length=1100

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||  
 Sbjct 606 TGAAGTTGGGCTCGAACCC 588

>emb|X13709.1|HSPEROXR **UG** Human gpx1 mRNA for glutathione peroxidase  
 Length=819

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||  
 Sbjct 327 TGAAGTTGGGCTCGAACCC 309

>ref|NM\_001085444.1| **UG** Oryctolagus cuniculus glutathione peroxidase 1 (GPX1),  
 emb|X13837.1|OCGPO **UG** Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9)  
 Length=760

GENE ID: 100009258 GPX1 | glutathione peroxidase 1 [Oryctolagus cuniculus]  
 (10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 337 TGAAGTTGGGCTCGAACCC 319

>gb|M21304.1|HUMGLP **UG** Human glutathione peroxidase (GPX1) mRNA, complete cds  
 Length=856

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 363 TGAAGTTGGGCTCGAACCC 345

>emb|AJ010340.1|SAJ10340 **UG** Sus scrofa mRNA for glutathione peroxidase, partial  
 Length=348

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]  
 (10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 100 TGAAGTTGGGCTCGAACCC 82

>emb|CR626479.1| **UG** full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapi  
 (human)  
 Length=838

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 342 TGAAGTTGGGCTCGAACCC 324

>emb|CR620255.1| **UG** full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50  
 of Homo sapiens (human)  
 Length=828

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
 (Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
 Identities = 19/19 (100%), Gaps = 0/19 (0%)  
 Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
 |||||  
 Sbjct 351 TGAAGTTGGGCTCGAACCC 333

>emb|CR614747.1| **UG** full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-norm  
of Homo sapiens (human)  
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 376 TGAAGTTGGGCTCGAACCC 358

>emb|CR601795.1| **UG** full-length cDNA clone CS0DI068YJ17 of Placenta Cot 25-norm  
of Homo sapiens (human)  
Length=792

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 296 TGAAGTTGGGCTCGAACCC 278

>emb|CR595371.1| **UG** full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25  
of Homo sapiens (human)  
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 353 TGAAGTTGGGCTCGAACCC 335

>dbj|AK130160.1| **UG** Homo sapiens cDNA FLJ26650 fis, clone MPE04848, highly simi  
to Glutathione peroxidase (EC 1.11.1.9)  
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||  
Sbjct 369 TGAAGTTGGGCTCGAACCC 351

>gb|AC121247.2| **U** Homo sapiens chromosome 3 clone RP11-3B7, complete sequence  
Length=170787

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19

Sbjct 23229 |||||TGAAGTTGGGCTCGAACCC 23211

>dbj|AB105162.1| Macaca fuscata mRNA for cytosolic glutathione peroxidase, compl  
cds  
Length=606

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||TGAAGTTGGGCTCGAACCC 304  
Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>ref|NM\_000581.2| **UEG** Homo sapiens glutathione peroxidase 1 (GPX1), transcript  
1, mRNA  
Length=921

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||TGAAGTTGGGCTCGAACCC 390  
Sbjct 408 TGAAGTTGGGCTCGAACCC 390

>ref|NM\_201397.1| **UEG** Homo sapiens glutathione peroxidase 1 (GPX1), transcript  
2, mRNA  
Length=1200

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17  
Identities = 19/19 (100%), Gaps = 0/19 (0%)  
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19  
|||||TGAAGTTGGGCTCGAACCC 669  
Sbjct 687 TGAAGTTGGGCTCGAACCC 669

>ref|XM\_001788272.1| **UG** PREDICTED: Bos taurus hypothetical protein LOC100139030  
mRNA  
Length=761

GENE ID: 100139030 LOC100139030 | hypothetical protein LOC100139030  
[Bos taurus]

Score = 34.2 bits (17), Expect = 2.6  
Identities = 17/17 (100%), Gaps = 0/17 (0%)  
Strand=Plus/Plus

Query 3 AAGTTGGGCTCGAACCC 19  
|||||AAGTTGGGCTCGAACCC 520  
Sbjct 504 AAGTTGGGCTCGAACCC 520

>ref|NM\_174076.3| **UG** Bos taurus glutathione peroxidase 1 (GPX1), mRNA  
Length=926

GENE ID: 281209 GPX1 | glutathione peroxidase 1 [Bos taurus]  
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6  
Identities = 17/17 (100%), Gaps = 0/17 (0%)